

Clustering Drives Assortativity and Community Structure in Ensembles of Networks

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(Dated: January 6, 2011)

Clustering, assortativity, and communities are key features of complex networks. We probe dependencies between these attributes and find that ensembles with strong clustering display both high assortativity by degree and prominent community structure, while ensembles with high assortativity are much less biased towards clustering or community structure. Further, clustered networks can amplify small homophilic bias for trait assortativity. This marked asymmetry suggests that transitivity, rather than homophily, drives the standard nonsocial/social network dichotomy.

PACS numbers: 89.75.Hc, 05.10.Ln, 89.75.Fb, 64.60.aq

Networks provide convenient representations for diverse phenomena spanning physical, technological, social, biological and informational domains [1–4]. They are often complicated, historically contingent assemblies created by nonlinear processes. Just as it is meaningful to “explain” features of real networks with simple generative mechanisms, it is also informative to ask what properties to expect given no other information about a network save that it has a certain set of properties.

In fact, network properties can be markedly interdependent [5, 6]. We focus on three key features of undirected networks: (1) the clustering coefficient, C , which reflects the tendency of the network to form triangles (transitivity) [7, 8]; (2) the assortativity, r , which reflects the tendency of similar nodes to connect to one another (homophily) [9]; and (3) the modularity, Q , which reflects the tendency of nodes to form tightly interconnected communities [10].

We show that ensembles of networks constrained by a transitive bias to be strongly clustered also become highly degree-assortative and modular. In contrast, ensembles constrained by a homophilic bias to be highly assortative show only weak clustering or modularity. Hence, at the ensemble level a fundamental asymmetry exists between transitivity and homophily. This asymmetry holds unless the distribution of the number of links attached to each node (the node’s degree) is extremely broad. Furthermore, a transitive bias can amplify the effect of a homophilic bias towards trait (i.e. race, age, education, etc.) assortativity [11] in network ensembles.

High values for the clustering, assortativity, and modularity are often observed in real-world social networks, while nonsocial networks may have low values [12]. Although extensive social science literature posits homophily to be a dominant force in social network formation [11, 13] (since social networks are highly assortative), our results show that a bias for transitive relationships (also called “triadic closure” in sociology literature [14])

is sufficient to obtain this effect in network ensembles. Our work is complementary to that of Newman and Park who produce assortativity and clustering characteristic of social networks by introducing modularity [12].

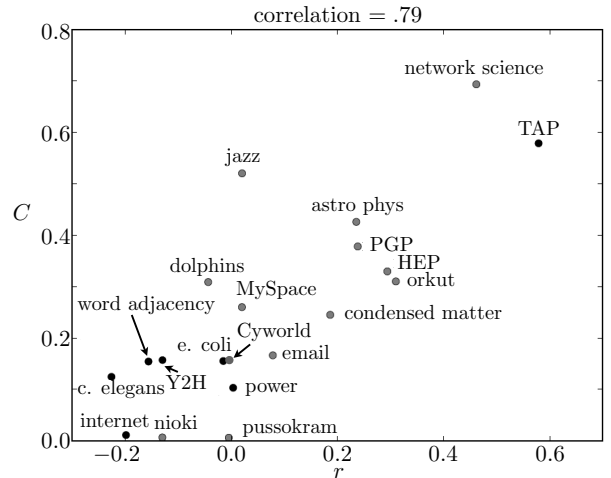


FIG. 1: The relationship between the clustering coefficient, C , and the assortativity, r . Gray points represent social networks, black points represent other types of networks. **Social networks:** astro phys (scientific collaboration) [15]; condensed matter (scientific collaboration) [15]; Cyworld (online social) [16]; dolphins (friendship) [17]; email (communication) [18]; HEP (scientific collaboration) [15]; jazz (musical collaboration) [19]; MySpace (online social) [16]; network science (scientific collaboration) [20]; nioki (online social) [21]; orkut (online social) [16]; PGP (communication network) [22]; pussokram (online dating) [21]. **Non-social networks:** c. elegans (neural) [23]; e. coli (metabolic) [24]; internet (router level) [25]; power (connections between power stations) [7]; TAP (yeast protein-protein binding) [26]; word adjacency (in English text) [20]; Y2H (yeast protein-protein binding) [27].

To begin, we note a distinct empirical correlation between C and r in real networks illustrated in Fig. 1, with social networks (generally) in the high C , high r corner, and non-social networks (generally) in the low C , low r one. The pattern suggests an interdependence between the two features that transcends a simple nonsocial-

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TABLE I: Important values for the empirical networks

Name	N	L	r	C	Q	Ref
ER	19680	41000	-1.3e-5	.00021	.246	[31]
HEP	7610	15751	.29	.33	.40	[15]
NetSci	1461	2742	.46	.70	.47	[20]
PGP	10680	24316	.24	.38	.41	[22]

cial/social dichotomy. For instance, consider two networks in Fig. 1: TAP is a high C , high r protein-protein interaction network, generated by tandem affinity purification experiments [28]; Y2H is a *weakly* clustered, *disassortative* protein-protein interaction network, generated using yeast two hybridization [29]. The experimental methodology, by itself, can explain the difference, since TAP pulls out bound complexes and assigns links to every pair of proteins in the complex while Y2H tests each pair of proteins individually for direct binding. Since transitivity has a natural origin in the construction of the TAP network, it is likely that the observed assortativity arises solely as a byproduct of the interrelationship between transitivity and assortativity rather than any direct homophilic tendency between proteins.

Since network properties often depend conspicuously on the degree sequence – or the number of links attached to each node [30] – we consider ensembles of networks constrained to have the same fixed degree sequence (FDS). Three real world networks are studied in detail: a collaboration network of high energy physicists (HEP) [15]; a collaboration network of network scientists (NetSci) [20]; and an encrypted communication network (PGP) [22]. We also examine a randomly generated Erdős - Rényi network (ER) [31]. Basic network parameters are given in Table I.

We use a rewiring procedure [32, 33] to sample from each ensemble. At each step of the procedure two links are chosen at random and their endpoints are exchanged, unless this would create a double link, in which case the step is skipped. This move set preserves the degree of each node but otherwise randomizes connections. To sample ensembles with specific features, we use a network Hamiltonian $H(G)$ [34–37] to define an exponential ensemble by assigning a sampling weight $P(G) \propto e^{-H(G)}$ to each graph G . Here we consider ensembles where $H(G)$ depends on C , r and/or trait assortativity defined below. Denoting the number of triangles in G by n_Δ , the degree of node i by k_i , and the number of nodes by N , the clustering coefficient is defined as

$$C = \frac{3n_\Delta}{\frac{1}{2} \sum_{i=1}^N (k_i - 1)k_i} . \quad (1)$$

Assortativity by degree is defined as the Pearson correlation coefficient between the degrees of nodes joined by a link [9]:

$$r = \frac{L \sum_{i=1}^L j_i k_i - [\sum_{i=1}^L j_i]^2}{L \sum_{i=1}^L j_i^2 - [\sum_{i=1}^L j_i]^2} , \quad (2)$$

where L is the number of links in the network and j_i and k_i are the degrees of nodes at each end of link i .

To get ensembles with specific values of C or r we use the following Hamiltonians:

$$H_{C'} = \beta|C' - C_t|, \quad H_{r'} = \beta|r' - r_t| , \quad (3)$$

where C' is the current clustering coefficient and C_t is the target value, and similarly for r' . The parameter β controls the strength of bias towards the target. It is a transitive bias in $H_{C'}$ and a homophilic bias in $H_{r'}$.

We employ simulated annealing based on a standard Metropolis-Hastings procedure with a rewiring move set [38, 39]. One pair of links in the network G is switched to produce a new candidate network G' . A valid move is accepted with probability

$$p = e^{H(G) - H(G')} \quad p \leq 1 , \quad (4)$$

and rejected with probability $1 - p$. If $p > 1$ the move is accepted. Initially, the network is rewired 2×10^5 times at $\beta = 0$ to randomize links and avoid strong hysteresis [37]. Then β is increased slowly, rewiring 5×10^4 times after each increase until C (or r) hits C_t (or r_t). The first network with $C = C_t$ ($r = r_t$) is a single sample from the ensemble of networks with a fixed degree sequence and $C = C_t$ ($r = r_t$). The whole process then repeats, starting with the $\beta = 0$ quench.

We also study the influence of transitivity on trait assortativity, r_d , which measures the tendency for nodes to connect to others with the same discrete trait (e.g. race, gender, etc.) [9]. For this we add a homophilic bias β_d for links between nodes with the same trait. Defining $r_d \propto \sum_\delta e_{\delta\delta}$, where $e_{\delta\delta}$ is the fraction of links in the network from a node of type δ to another node of type δ , the Hamiltonian becomes

$$H_d = \beta|C - C_t| + \beta_d \sum_\delta e_{\delta\delta} . \quad (5)$$

Choosing different values of C_t and β_d allows one to explore how transitivity impacts trait assortativity at the ensemble level.

We examine ensembles constrained to have a particular value of r (resp. C) and measure the value for the other feature C (resp. r) averaged over 100 samples from the ensemble. Results are shown in Fig. 2. The grey (resp. black) symbols show the values for ensembles with constrained r (resp. C). Increasing transitivity to increase C has a strong influence on r in all cases, whereas increasing homophily to increase r has relatively little impact on C . The asymmetry is strongest for narrow degree distributions (e.g. the ER network), and becomes less pronounced, but still apparent, as the degree distribution broadens.

The asymmetric relationship between r and C can be understood as follows: For nodes to participate in as many transitive relationships as possible, their neighbours must be of similar degree. Hence increasing clus-

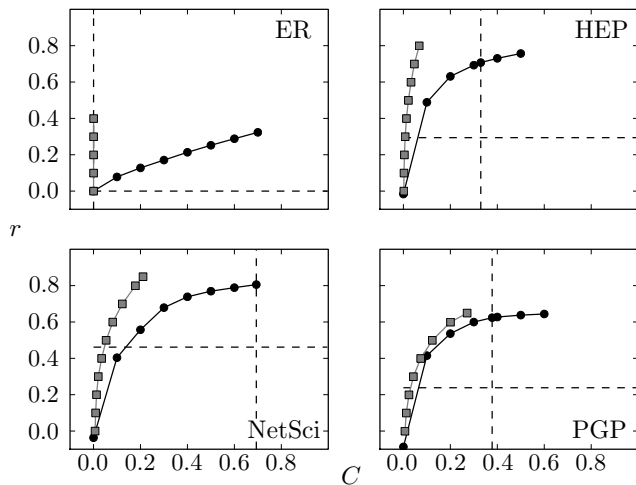


FIG. 2: Controlling assortativity (grey symbols) vs. controlling clustering coefficient (black symbols) for various network degree sequences. C is on the x -axis, r on the y -axis. Each point represents average values from 100 samples from an ensemble with specified r or C values. The dashed lines show the values of r and C for the original network. Note the asymmetry between the effect of C on r compared to r on C .

tering also increases r . Increasing r leads to links between nodes of similar degree, but these relationships need not be transitive. For narrow degree distributions, one could divide all nodes of degree k into two groups and only permit links between the two groups. Assortativity would be maximum, in the absence of any clustering.

On the other hand, for broad degree distributions (like PGP) only a few nodes of high degree exist, but they have a large effect on r . Hence for large r , the highest degree nodes are under strong pressure to link, thus creating many transitive relationships. Many social networks do not have broad degree distributions. In such cases homophily has only a weak influence on C at the ensemble level.

Fig. 2 also indicates the C and r values for the real-world networks (dashed lines). Ensembles of networks constrained to have the same C as the real network exhibit far greater r . Hence, social networks are actually *disassortative* relative to the ensemble of networks with the same clustering coefficient and degree sequence [40]. Indeed, the most likely way to create many triangles is to densely interconnect the higher degree nodes so triangles clump together (as discussed in Ref. [37]). Real social networks seem to spread clustering more evenly across the network, thus lowering r . For example in scientific collaboration networks, supervisory relationships may decrease the assortativity by creating links between lower degree students and higher degree professors.

We next consider the influence of r and C on modularity. Many methods for extracting community structure exist [41, 42]. For definiteness, we use the one proposed by Newman and Girvan [10]: Given a partition of the network, e_{ij} is the fraction of all edges connecting a node in community i to one in community j , and $a_i = \sum_j e_{ij}$

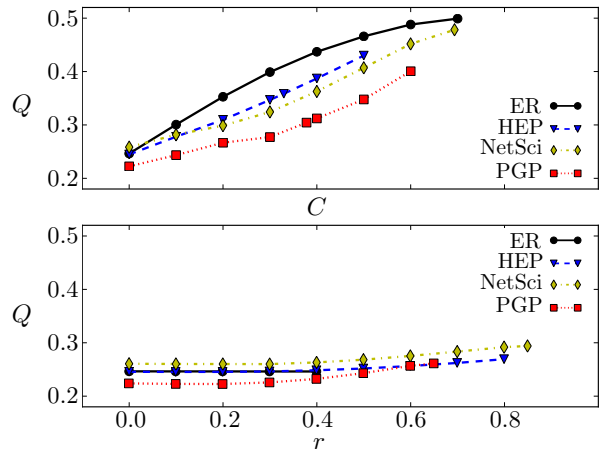


FIG. 3: (Color Online) Modularity Q for various ensembles of networks with different target values for C (top row) or r (bottom row). Clustering has a much larger impact on modularity than assortativity does.

is the fraction of all links within community i . The modularity of the network given partition \mathcal{P} is defined as:

$$Q_{\mathcal{P}} = \sum_i (e_{ii} - a_i^2) \quad (6)$$

We use an agglomerative method [43] to approximate the best partition and largest $Q_{\mathcal{P}}$, which we denote Q .

The top (resp. bottom) panel in Fig. 3 shows the average Q in ensembles with constrained C (resp. r). Transitivity has a more pronounced effect on modularity than does homophily. The modularity achieved for the highly clustered ensembles approximates the actual modularity for the real networks (HEP, NetSci, and PGP; see Table I), unlike assortative ensembles without a transitive bias.

Finally, we consider the effect of transitivity on trait assortativity, r_d . For each of the degree sequences, we create ensembles of networks with different target C values and varying homophilic biases β_d . Since the actual data sets do not contain trait values, we assign each node one of three possible traits at random with equal probability. For ER, HEP, and NetSci we observe that ensembles with larger C enhance r_d relative to ensembles with the same homophilic bias but no clustering ($C = 0$). This is especially clear for the narrowest (ER) degree sequence. For the PGP network, which has a broad degree distribution, clustering appears to compete with the homophilic bias (e.g. the curves cross), leading to a more complicated scenario. The interdependence between clustering and trait assortativity thus appears to depend on the degree sequence, but for narrow degree sequences the positive relationship holds and transitivity enhances the effect of homophilic bias. We also note that increasing the trait assortativity of an ensemble had no impact on C , r , or Q (data not shown).

We conjecture that the standard nonsocial/social (dis-

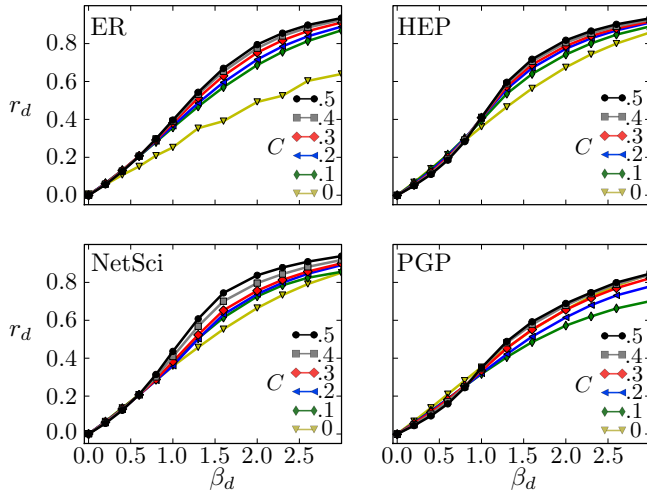


FIG. 4: (Color Online) Trait assortativity r_d (y-axis) for ensembles of networks with varying C (indicated in the legend) and homophilic bias β_d (x-axis). For narrow degree distributions clustering amplifies the response of trait assortativity on homophilic bias. For broad degree distribution the opposite occurs for small β_d .

assortative/assortative) dichotomy is driven by transitive relationships in many social networks, such as in scientific collaborations. As shown here, transitivity typically leads to assortativity. This explains the anomalous position of TAP located within social networks, and is consistent with another anomaly in Fig. 1: several online social networks show low clustering and low assortativity [44]. If assortative mixing by degree is the result of homophily by degree in social networks, this anomaly is hard to explain: why should popular people stop seeking each other out simply because the social network moved online? But if assortativity is a side-effect of transitivity, this effect is easier to understand: it is plausible that online social relationships are less transitive, since in the absence of spatially mediated interactions there is a smaller tendency to introduce mutual friends. We have not ruled out the scenario in reference [12]. Indeed, the causal factors driving network evolution are likely to be complex, multifaceted, and idiosyncratic. Our results on the asymmetric dependencies between clustering, assortativity, and modularity provide a warning about inferring causality from naive observations of network structure.

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